

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
- (ii) TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
- (iii) NUMBER OF SEQUENCES: 51
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: P.O. Box 4433
 - (C) CITY: Houston
 - (D) STATE: TX
 - (E) COUNTRY: USA
 - (F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US UNKNOWN
 - (B) FILING DATE:
 - (C) CLASSIFICATION: UNKNOWN
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/038,118
 - (B) FILING DATE: 20-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hibler, David W.
 - (B) REGISTRATION NUMBER: 41,071
 - (C) REFERENCE/DOCKET NUMBER: UTXC:506
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 512/418-3000
 - (B) TELEFAX: 512/474-7577

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	

TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu 160 165 170	528
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val 175 180 185 190	576
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu 195 200 205	624
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val 210 215 220	672
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro 225 230 235	720
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg 240 245 250	768
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp 255 260 265 270	816
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp 275 280 285	864
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser 290 295 300	912
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser 305 310 315	960
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg 320 325 330	1008
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser 335 340 345 350	1056
TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val 355 360 365	1104

AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC	1152
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile	
370 375 380	
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA	1200
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu	
385 390 395	
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT	1248
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser	
400 405 410	
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT	1296
Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe	
415 420 425 430	
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC	1344
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr	
435 440 445	
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA	1392
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys	
450 455 460	
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT	1440
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn	
465 470 475	
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA	1488
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val	
480 485 490	
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA	1536
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr	
495 500 505 510	
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT	1584
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe	
515 520 525	
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1632
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
530 535 540	
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1680
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
545 550 555	
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1728
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
560 565 570	

CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1776
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
575 580 585 590	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1824
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
595 600 605	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1872
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
610 615 620	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1920
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
625 630 635	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1968
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
640 645 650	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	2016
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
655 660 665 670	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	2064
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
675 680 685	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	2112
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
690 695 700	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	2160
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
705 710 715	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	2208
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
720 725 730	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	2256
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
735 740 745 750	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	2304
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
755 760 765	
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA	2352
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile	
770 775 780	

CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2400
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg	
785 790 795	
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA	2448
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys	
800 805 810	
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA	2496
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg	
815 820 825 830	
ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG	2544
Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln	
835 840 845	
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT	2592
Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser	
850 855 860	
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT	2640
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp	
865 870 875	
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG	2688
Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu	
880 885 890	
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA	2736
Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg	
895 900 905 910	
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA	2784
Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu	
915 920 925	
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG	2840
Glu Lys	
TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2900
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2960
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTA AATCCTGCCA	3020
TTTAAAAAGT TGTCAGAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	3080
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3140
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	3200
TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA	3260

TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	3320
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3380
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3440
AACCATATGA TACTATCATA CTACTGAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT	3500
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGTC	3555

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	1	5	10	15
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	20	25	30	
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	35	40	45	
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	50	55	60	
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	65	70	75	80
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	85	90	95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	100	105	110	
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	115	120	125	
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	130	135	140	
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	145	150	155	160
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	165	170	175	

Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	180	185	190
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	195	200	205
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	210	215	220
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	225	230	235
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	245	250	255
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	260	265	270
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	275	280	285
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	290	295	300
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	305	310	315
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	325	330	335
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	340	345	350
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	355	360	365
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	370	375	380
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	385	390	395
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	405	410	415
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	420	425	430
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	435	440	445
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	450	455	460

Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	
465					470					475					480	
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	
			485						490					495		
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	
			500					505					510			
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	
		515					520					525				
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	
	530					535					540					
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	
545					550					555					560	
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	
			565						570					575		
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	
			580					585					590			
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	
		595					600					605				
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	
	610					615						620				
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	
625					630					635					640	
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	
				645					650					655		
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	
			660					665					670			
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	
		675					680					685				
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	
	690					695					700					
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	
705					710					715					720	
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	
				725					730					735		
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	
			740					745					750			

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile	755	760	765
Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His	770	775	780
Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro	785	790	795 800
Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser	805	810	815
Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu	820	825	830
Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile	835	840	845
Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu	850	855	860
Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu	865	870	875 880
Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys	885	890	895
Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln	900	905	910
Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	915	920	925

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGTC ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
1 5 10	

AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	96
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
15 20 25 30	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	144
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
35 40 45	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	192
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
50 55 60	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	240
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
65 70 75	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	288
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
80 85 90	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	336
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
95 100 105 110	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	384
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
115 120 125	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	432
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
130 135 140	
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	480
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
145 150 155	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	528
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
160 165 170	
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT	576
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser	
175 180 185 190	
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT	624
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser	
195 200 205	
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA	672
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg	
210 215 220	

TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT	720
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser	
225 230 235	
TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG	768
Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val	
240 245 250	
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC	816
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile	
255 260 265 270	
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA	864
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu	
275 280 285	
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT	912
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser	
290 295 300	
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT	960
Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe	
305 310 315	
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC	1008
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr	
320 325 330	
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA	1056
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys	
335 340 345 350	
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT	1104
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn	
355 360 365	
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA	1152
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val	
370 375 380	
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA	1200
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr	
385 390 395	
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT	1248
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe	
400 405 410	
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1296
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
415 420 425 430	

ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1344
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
435 440 445	
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1392
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
450 455 460	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1440
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
465 470 475	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1488
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
480 485 490	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1536
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
495 500 505 510	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1584
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
515 520 525	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1632
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
530 535 540	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	1680
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
545 550 555	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	1728
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
560 565 570	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	1776
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
575 580 585 590	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	1824
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
595 600 605	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	1872
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
610 615 620	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	1920
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
625 630 635	

TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr 640 645 650	1968
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile 655 660 665 670	2016
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg 675 680 685	2064
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys 690 695 700	2112
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg 705 710 715	2160
ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln 720 725 730	2208
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser 735 740 745 750	2256
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp 755 760 765	2304
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu 770 775 780	2352
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg 785 790 795	2400
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu 800 805 810	2448
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG Glu Lys 815	2504
TCTCTCACAG ATGTGACTGT ATAACCTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2564
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2624
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	2684

TTTAAAAAGT TGTAGCAGAT TGTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	2744
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	2804
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	2864
TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA	2924
TTGACTGCCC ATTACACAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	2984
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3044
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3104
AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT	3164
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3218

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val	
1 5 10 15	
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val	
20 25 30	
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala	
35 40 45	
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln	
50 55 60	
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys	
65 70 75 80	
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met	
85 90 95	
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp	
100 105 110	
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys	
115 120 125	

Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	130	135	140	
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	145	150	155	160
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	165	170	175	
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	180	185	190	
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	195	200	205	
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	210	215	220	
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	225	230	235	240
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	245	250	255	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	260	265	270	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	275	280	285	
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	290	295	300	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	305	310	315	320
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	325	330	335	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	340	345	350	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	355	360	365	
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	370	375	380	
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	385	390	395	400
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	405	410	415	

Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	420	425	430	
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	435	440	445	
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	450	455	460	
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	465	470	475	480
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	485	490	495	
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	500	505	510	
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	515	520	525	
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	530	535	540	
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	545	550	555	560
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	565	570	575	
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	580	585	590	
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	595	600	605	
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	610	615	620	
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	625	630	635	640
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	645	650	655	
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	660	665	670	
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	675	680	685	
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	690	695	700	

Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu
705					710					715					720
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile
			725						730					735	
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu
			740					745					750		
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu
		755					760					765			
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
		770				775					780				
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
785					790					795					800
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
				805					810					815	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCGAGCAAT GGGCGTGATA GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCATT	60
GACGTCAATG GGAGTTTGTGTT TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC	120
AACTCCGCCC CATTGACGCA AATGGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC	180
AGAGCTCGTT TAGTGAACCG TCAGATCGCC TGGAGACGCC ATCCACGCTG TTTTGACCTC	240
CATAGAAGAC ACCGGGACCG ATCCAGCCTC CGCGGCCGCG AATTC	285

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTCGAGC AATGGGCGTG GATAGCGG	28
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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGCTCGAGC ACCAAAATCA ACGGGA

26

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGCTCGAGC AACTCCGCCC CATTGAC

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAGACATATG AATTGCGGC C

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAGAATTCG CTGTCTGCG

19

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTCTAGATG CAGTTGGACC TGGGAG

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCAAGCTTG CCGCCATGTC GTTCACTTTT AC

32

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCCAAGAGA ATTCATAAAA GG

22

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCAAGCTTG CCGCCATGGA GCAGGACAGC GGCCCCGGAC

39

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCAAGCTTG CCGCCATGGA TTTTACTGCA TTATGTCAG 39

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCAAGCTTG CCGCCATGGA GAAAGTTTCA TCTTGTGAT 39

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAAGCTTG CCGCCATGCT GTGGGGAATC TGTATCTTT 39

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCAAGCTTG CCGCCATGTC AAGACTGTTG AAGAAG 36

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCGCCTGAGG ACCTAGATGA GATGTCGTTTC 30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGGTTAACC CTAGATGAGA TGTCGTTTAC T 31

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCCAAGCTTG CCGTCATGCC GCCCAAAACC CCCC GA 36

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCACCTAGG TCAACTGCTG CAAT 24

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTTGACCTAG GTGATATGTC GTTC

24

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGCCTAGGA TCTACTGAAA TAAATTCTGC A

31

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCCGATATCA ACTGCTGGGT TGTGTCAAAT A

31

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCGAATTCG TTTTATATGG TTCTTTGAGC AA

32

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 4..5
- (D) OTHER INFORMATION: /note= "R=A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCCRCCAUGG

10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCCGTC ATG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG CTT	48
Met Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu	
1 5 10	
GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG AAA	96
Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys	
15 20 25 30	
TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG GAG	144
Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu	
35 40 45	
AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG AAA	192
Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys	
50 55 60	
AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA GAT	240
Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp	
65 70 75	

GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC AGT	288
Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser	
80 85 90	
GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC AAA	336
Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys	
95 100 105 110	
GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT	384
Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe	
115 120 125	
GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA	432
Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr	
130 135 140	
CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA	480
Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu	
145 150 155	
AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA	528
Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln	
160 165 170	
ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT	576
Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu	
175 180 185 190	
GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT	624
Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr	
195 200 205	
AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA	672
Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg	
210 215 220	
GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA	720
Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr	
225 230 235	
AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG	768
Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu	
240 245 250	
GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT	816
Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu	
255 260 265 270	
GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA	864
Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys	
275 280 285	

CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA	912
Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu	
290 295 300	
TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT	960
Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe	
305 310 315	
GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT	1008
Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn	
320 325 330	
GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA	1056
Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln	
335 340 345 350	
CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT	1104
Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn	
355 360 365	
CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA	1152
Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile	
370 375 380	
CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT	1200
Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala	
385 390 395	
AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA	1248
Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys	
400 405 410	
CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA	1296
Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser	
415 420 425 430	
GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC	1344
Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp	
435 440 445	
AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG	1392
Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met	
450 455 460	
GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT	1440
Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp	
465 470 475	
TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT	1488
Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp	
480 485 490	

TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA	1536
Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr	
495 500 505 510	
AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA	1584
Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu	
515 520 525	
TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA	1632
Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln	
530 535 540	
TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT	1680
Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro	
545 550 555	
CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT	1728
Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu	
560 565 570	
TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT	1776
Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn	
575 580 585 590	
TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG	1824
Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln	
595 600 605	
AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT	1872
Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr	
610 615 620	
CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT	1920
Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser	
625 630 635	
GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC	1968
Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr	
640 645 650	
CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT	2016
Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile	
655 660 665 670	
ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT	2064
Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu	
675 680 685	
AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT	2112
Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val	
690 695 700	

CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser 705 710 715	2160
ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn 720 725 730	2208
ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro 735 740 745 750	2256
CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile 755 760 765	2304
CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile 770 775 780	2352
TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile 785 790 795	2400
TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys 800 805 810	2448
ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala 815 820 825 830	2496
GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile 835 840 845	2544
GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser 850 855 860	2592
AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met 865 870 875	2640
CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu 880 885 890	2688
AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG Lys 895	2741
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2801

TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2861
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	2921
TTTAAAAAGT TGTCAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	2981
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3041
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	3101
TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA	3161
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	3221
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3281
ACTGTGTGCT TGTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3341
AACCATATGA TACTATCATA CTA CTGAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT	3401
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3455

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	Phe
1				5				10					15		
Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	Lys
			20					25					30		
Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	Val
			35					40					45		
Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	Glu
		50				55					60				
Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	Met
65					70					75				80	
Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	His
				85						90				95	
Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	Asp
			100					105					110		

Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	Leu		
		115					120					125					
Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	Pro		
		130				135					140						
Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val		
145					150					155					160		
Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu		
				165					170					175			
Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr		
			180					185					190				
Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr		
		195					200					205					
Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln		
		210				215					220						
Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile		
225					230					235					240		
Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys		
				245				250						255			
Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu		
			260					265						270			
Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr		
			275				280						285				
Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu		
		290				295					300						
Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr		
305					310					315					320		
Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile		
				325					330					335			
Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu		
			340					345						350			
Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile		
		355					360					365					
Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys		
		370				375					380						
Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala		
385					390					395					400		

Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly
405 410 415

Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu
420 425 430

Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile
435 440 445

Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr
450 455 460

Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser
465 470 475 480

Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr
485 490 495

Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu
500 505 510

Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu
515 520 525

Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys
530 535 540

Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn
545 550 555 560

Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro
565 570 575

Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr
580 585 590

Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro
595 600 605

Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu
610 615 620

Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His
625 630 635 640

Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln
645 650 655

Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met
660 665 670

Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe
675 680 685

Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu
 690 695 700
 Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile
 705 710 715 720
 Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu
 725 730 735
 Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile
 740 745 750
 Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly
 755 760 765
 Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu
 770 775 780
 Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val
 785 790 795 800
 Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn
 805 810 815
 Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly
 820 825 830
 Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly
 835 840 845
 Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe
 850 855 860
 Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys
 865 870 875 880
 Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
 885 890 895

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCATC ATG GAT TTT ACT GCA TTA TGT CAG AAA TTA AAG ATA CCA GAT	48
Met Asp Phe Thr Ala Leu Cys Gln Lys Leu Lys Ile Pro Asp	
1 5 10	
CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG GAG AAA GTT TCA TCT GTG	96
His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys Val Ser Ser Val	
15 20 25 30	
GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG AAA AAG GAA CTG TGG GGA	144
Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys Glu Leu Trp Gly	
35 40 45	
ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA GAT GAG ATG TCG TTC ACT	192
Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu Met Ser Phe Thr	
50 55 60	
TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC AGT GTC CAT AAA TTC TTT	240
Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val His Lys Phe Phe	
65 70 75	
AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC AAA GTT GAT AAT GCT ATG	288
Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val Asp Asn Ala Met	
80 85 90	
TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT GCA CTC TTC AGC AAA	336
Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala Leu Phe Ser Lys	
95 100 105 110	
TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA CAA CCC AGC AGT TCG	384
Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln Pro Ser Ser Ser	
115 120 125	
ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT TCT TGG ATC	432
Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val Ser Trp Ile	
130 135 140	
ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA GAT GAT CTG	480
Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu Asp Asp Leu	
145 150 155	
GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT TTT ATT AAA	528
Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr Phe Ile Lys	
160 165 170	
CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA GCT GTT ATA	576
Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr Ala Val Ile	
175 180 185 190	
CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG AGT	624
Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg Ser	
195 200 205	

GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA GTT	672
Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu Val	
210 215 220	
CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT TAT	720
Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val Tyr	
225 230 235	
TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA TCT	768
Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser	
240 245 250	
AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA ATT	816
Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile	
255 260 265 270	
TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT GAT	864
Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp	
275 280 285	
AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA ACA	912
Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr	
290 295 300	
CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA CAC	960
Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro His	
305 310 315	
ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG ATT	1008
Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met Ile	
320 325 330	
TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT	1056
Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe	
335 340 345 350	
AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG	1104
Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys	
355 360 365	
GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA CAG	1152
Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln	
370 375 380	
GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC TTG	1200
Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu	
385 390 395	
TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA GAA CGA TTA	1248
Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu	
400 405 410	

TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT TTT CAT ATG	1296
Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met	
415 420 425 430	
TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC AGA	1344
Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg	
435 440 445	
AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA TGG	1392
Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp	
450 455 460	
ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC	1440
Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile	
465 470 475	
GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA ATG ATA AAA	1488
Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys	
480 485 490	
CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT GCA TGG CTC	1536
His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu	
495 500 505 510	
TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA GAA	1584
Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu	
515 520 525	
GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT CTC	1632
Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu	
530 535 540	
CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT	1680
Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser	
545 550 555	
CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT GCA	1728
Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala	
560 565 570	
GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT	1776
Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser	
575 580 585 590	
ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC	1824
Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu	
595 600 605	
CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA	1872
Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu	
610 615 620	

GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT	1920
Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr	
625 630 635	
GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG	1968
Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser Met	
640 645 650	
TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT	2016
Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile	
655 660 665 670	
GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA	2064
Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys	
675 680 685	
CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT	2112
Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr	
690 695 700	
AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT	2160
Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala	
705 710 715	
TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC	2208
Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser	
720 725 730	
CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC	2256
Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile	
735 740 745 750	
TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA	2304
Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro	
755 760 765	
ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT	2352
Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly	
770 775 780	
GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA	2400
Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val	
785 790 795	
TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT	2448
Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro	
800 805 810	
CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT GAA	2496
Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu	
815 820 825 830	

GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA	2544
Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys	
835 840 845	
CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG	2592
Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met	
850 855 860	
AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC	2638
Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
865 870	
AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT	2698
ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA	2758
TAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG	2818
TTATTTATAC AAGATTGAAA ATCTTG TGTA AATCCTGCCA TTTAAAAAGT TG TAGCAGAT	2878
TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT	2938
GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG	2998
ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC	3058
TTAGAAAATG TGCCTATCT ATCTTCCAAA TGCAATTGA TTGACTGCCC ATTCACCAAA	3118
ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT	3178
TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTTATAA	3238
AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA	3298
CTACTGAAAC AGATTTCATA CCTCAGAATG TAAAAGAACT TACTGATTAT TTTCTTCATC	3358
CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3392

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Asp Phe Thr Ala Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val
1 5 10 15

Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly
			20					25					30		
Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys
			35					40					45		
Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr
			50					55					60		
Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu
			65					70					75		
Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg
			85					90					95		
Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu
			100					105					110		
Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser
			115					120					125		
Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe
			130					135					140		
Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile
			145					150					155		
Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser
			165					170					175		
Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile
			180					185					190		
Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg
			195					200					205		
Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys
			210					215					220		
Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys
			225					230					235		
Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly
			245					250					255		
Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu
			260					265					270		
Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr
			275					280					285		
Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg
			290					295					300		

Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr Pro
305 310 315 320

Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn
325 330 335

Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn
340 345 350

Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile
355 360 365

Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys
370 375 380

Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr
385 390 395 400

Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile
405 410 415

Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu
420 425 430

Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr
435 440 445

Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu
450 455 460

Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser
465 470 475 480

Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu
485 490 495

Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp
500 505 510

Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro
515 520 525

Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn
530 535 540

Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys
545 550 555 560

Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr
565 570 575

Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser
580 585 590

Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu
595 600 605

Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu Glu His
610 615 620

Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu
625 630 635 640

Met Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly
645 650 655

Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr
660 665 670

Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val
675 680 685

Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser
690 695 700

Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr
705 710 715 720

Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr
725 730 735

Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile
740 745 750

Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro
755 760 765

Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser
770 775 780

Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn
785 790 795 800

Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys
805 810 815

Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp
820 825 830

Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala
835 840 845

Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp
850 855 860

Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
865 870

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCATC ATG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	48
Met Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
1 5 10	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	96
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
15 20 25 30	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	144
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
35 40 45	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	192
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
50 55 60	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	240
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
65 70 75	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	288
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
80 85 90	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	336
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
95 100 105 110	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	384
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
115 120 125	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	432
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
130 135 140	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	480
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
145 150 155	

AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	528
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
160 165 170	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	576
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
175 180 185 190	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	624
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
195 200 205	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	672
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
210 215 220	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	720
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
225 230 235	
AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	768
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
240 245 250	
GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	816
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
255 260 265 270	
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	864
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
275 280 285	
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG	912
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met	
290 295 300	
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	960
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
305 310 315	
CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1008
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
320 325 330	
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1056
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
335 340 345 350	
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1104
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
355 360 365	

CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1152
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
370 375 380	
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1200
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
385 390 395	
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT	1248
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
400 405 410	
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1296
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
415 420 425 430	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1344
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
435 440 445	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1392
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
450 455 460	
GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1440
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
465 470 475	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1488
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
480 485 490	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1536
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
495 500 505 510	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1584
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
515 520 525	
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1632
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr	
530 535 540	
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC	1680
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala	
545 550 555	
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT	1728
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr	
560 565 570	

AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA	1776
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu	
575 580 585 590	
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT	1824
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu	
595 600 605	
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT	1872
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His	
610 615 620	
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG	1920
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys	
625 630 635	
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT	1968
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu	
640 645 650	
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG	2016
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu	
655 660 665 670	
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA	2064
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg	
675 680 685	
CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG	2112
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu	
690 695 700	
TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA	2160
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser	
705 710 715	
CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT	2208
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser	
720 725 730	
CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA	2256
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro	
735 740 745 750	
AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG	2304
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu	
755 760 765	
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC	2352
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu	
770 775 780	

AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA	2400
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu	
785 790 795	
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC	2448
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu	
800 805 810	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT	2496
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
815 820 825 830	
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA	2544
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser	
835 840 845	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT	2599
Asn Lys Glu Glu Lys	
850	
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC	2659
ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA	2719
TTCCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGCTGA	2779
AATCCTGCCA TTTAAAAAGT TGTCAGCAGT TGTTTCCTCT TCCAAAAGTAA AATTGCTGTG	2839
CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC	2899
TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT	2959
GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTTATCT ATCTTCCAAA	3019
TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAAATGGAT	3079
ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG	3139
AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA	3199
AGCAAAGTAT AACCATATGA TACTATCATA CTAAGTAAAC AGATTTTATA CCTCAGAATG	3259
TAAAAGAAGT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA	3319
TAGT	3323

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	
1				5					10					15		
Lys	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	
			20					25						30		
Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	
			35					40						45		
Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	
			50				55						60			
Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	
			65				70				75				80	
Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	
				85					90						95	
Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	
			100						105					110		
Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	
			115					120					125			
Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	
			130				135					140				
Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	
			145				150				155				160	
Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	
				165					170					175		
Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	
			180						185					190		
Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	
			195					200					205			
Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	
			210					215					220			

Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu
225 230 235 240

Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala
245 250 255

Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp
260 265 270

Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu
275 280 285

Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr
290 295 300

Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser
305 310 315 320

Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu
325 330 335

Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys
340 345 350

Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg
355 360 365

Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu
370 375 380

Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu
385 390 395 400

Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val
405 410 415

Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly
420 425 430

Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala
435 440 445

Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn
450 455 460

Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile
465 470 475 480

Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile
485 490 495

Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala
500 505 510

Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	515	520	525
Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	530	535	540
Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	545	550	555
Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	565	570	575
Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	580	585	590
Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	595	600	605
His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	610	615	620
Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	625	630	635
Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	645	650	655
Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	660	665	670
Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	675	680	685
Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	690	695	700
Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	705	710	715
Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	725	730	735
Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	740	745	750
Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	755	760	765
Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	770	775	780
Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	785	790	795

Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly
805 810 815

Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr
820 825 830

Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys
835 840 845

Glu Glu Lys
850

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCATC ATG CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	48
Met Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
1 5 10	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	96
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
15 20 25 30	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	144
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
35 40 45	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	192
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
50 55 60	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	240
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
65 70 75	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	288
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
80 85 90	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	336
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
95 100 105 110	

CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	384
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
115 120 125	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	432
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
130 135 140	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	480
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
145 150 155	
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	528
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
160 165 170	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	576
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
175 180 185 190	
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT	624
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser	
195 200 205	
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT	672
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser	
210 215 220	
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA	720
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg	
225 230 235	
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT	768
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser	
240 245 250	
TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG	816
Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val	
255 260 265 270	
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC	864
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile	
275 280 285	
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA	912
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu	
290 295 300	
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT	960
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser	
305 310 315	

ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe 320 325 330	1008
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr 335 340 345 350	1056
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys 355 360 365	1104
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn 370 375 380	1152
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val 385 390 395	1200
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr 400 405 410	1248
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe 415 420 425 430	1296
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu 435 440 445	1344
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met 450 455 460	1392
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys 465 470 475	1440
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys 480 485 490	1488
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr 495 500 505 510	1536
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val 515 520 525	1584

AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1632
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
530 535 540	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1680
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
545 550 555	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	1728
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
560 565 570	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	1776
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
575 580 585 590	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	1824
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
595 600 605	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	1872
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
610 615 620	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	1920
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
625 630 635	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	1968
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
640 645 650	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	2016
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
655 660 665 670	
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA	2064
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile	
675 680 685	
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2112
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg	
690 695 700	
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA	2160
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys	
705 710 715	
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA	2208
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg	
720 725 730	

[illegible]

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	
1				5					10						15	
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	
			20					25						30		
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	
			35				40						45			
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	
			50				55					60				
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	
			65			70				75					80	
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	
				85					90						95	
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	
			100					105						110		
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	
			115				120					125				
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	
			130			135					140					
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	
			145			150				155					160	
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	
				165					170					175		
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	
			180					185					190			
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	
			195				200					205				
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	
			210				215				220					

Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	225	230	235	240
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	245	250	255	
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	260	265	270	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	275	280	285	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	290	295	300	
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	305	310	315	320
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	325	330	335	
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	340	345	350	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	355	360	365	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	370	375	380	
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	385	390	395	400
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	405	410	415	
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	420	425	430	
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	435	440	445	
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	450	455	460	
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	465	470	475	480
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	485	490	495	
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	500	505	510	

Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	515	520	525	
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	530	535	540	
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	545	550	555	560
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	565	570	575	
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	580	585	590	
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	595	600	605	
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	610	615	620	
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	625	630	635	640
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	645	650	655	
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	660	665	670	
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	675	680	685	
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	690	695	700	
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	705	710	715	720
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	725	730	735	
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	740	745	750	
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	755	760	765	
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	770	775	780	
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys	785	790	795	800

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
805 810 815

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
820 825 830

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCCGTC ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT GCA CTC	48
Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala Leu	
1 5 10	
TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA CAA CCC	96
Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln Pro	
15 20 25 30	
AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT	144
Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val	
35 40 45	
TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA	192
Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu	
50 55 60	
GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT	240
Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr	
65 70 75	
TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA	288
Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr	
80 85 90	
GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG	336
Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln	
95 100 105 110	
AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT	384
Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile	
115 120 125	

ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys 130 135 140	432
AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu 145 150 155	480
GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr 160 165 170	528
GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu 175 180 185 190	576
GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr 195 200 205	624
CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile 210 215 220	672
CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu 225 230 235	720
ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile 240 245 250	768
TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys 255 260 265 270	816
AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala 275 280 285	864
GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly 290 295 300	912
GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu 305 310 315	960
GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile 320 325 330	1008

TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA	1056
Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr	
335 340 345 350	
TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT	1104
Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser	
355 360 365	
TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC	1152
Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr	
370 375 380	
AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA	1200
Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu	
385 390 395	
ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT	1248
Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu	
400 405 410	
GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG	1296
Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys	
415 420 425 430	
GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT	1344
Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn	
435 440 445	
CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT	1392
Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro	
450 455 460	
GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT	1440
Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr	
465 470 475	
GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA	1488
Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro	
480 485 490	
TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA	1536
Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu	
495 500 505 510	
GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC	1584
Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His	
515 520 525	
CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG	1632
Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln	
530 535 540	

AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG	1680
Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met	
545 550 555	
TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC	1728
Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe	
560 565 570	
AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG	1776
Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu	
575 580 585 590	
ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA	1824
Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile	
595 600 605	
GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG	1872
Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu	
610 615 620	
CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT	1920
Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile	
625 630 635	
CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA	1968
Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly	
640 645 650	
GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA	2016
Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu	
655 660 665 670	
GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA	2064
Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val	
675 680 685	
TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT	2112
Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn	
690 695 700	
CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA	2160
Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly	
705 710 715	
AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA	2208
Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly	
720 725 730	
TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT	2256
Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe	
735 740 745 750	

CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG	2304
Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys	
755 760 765	
CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA	2349
Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
770 775 780	
TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG	2409
ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT	2469
TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG	2529
TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT	2589
TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG	2649
GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG	2709
CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC	2769
ATGAACACCC TTAGAAAATG TGTCCTATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC	2829
ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAAATGGAT ATTATTAGAA ATTAGAAAAA	2889
AATTACTAAT TTTACACATT AGATTTTATT TTAATTATGG AATCTGATAT ACTGTGTGCT	2949
TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA	3009
TACTATCATA CTACTGAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT TACTGATTAT	3069
TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3113

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala Leu Phe Ser	
1 5 10 15	
Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln Pro Ser Ser	
20 25 30	
Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val Ser Trp	
35 40 45	

Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	50	55	60	
Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	65	70	75	80
Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	85	90	95	
Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	100	105	110	
Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	115	120	125	
Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	130	135	140	
Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	145	150	155	160
Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	165	170	175	
Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	180	185	190	
Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	195	200	205	
Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	210	215	220	
His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	225	230	235	240
Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	245	250	255	
Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	260	265	270	
Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	275	280	285	
Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	290	295	300	
Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	305	310	315	320
Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	325	330	335	

Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	340	345	350	
Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	355	360	365	
Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	370	375	380	
Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	385	390	395	400
Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	405	410	415	
Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	420	425	430	
Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	435	440	445	
Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	450	455	460	
Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	465	470	475	480
Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	485	490	495	
Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	500	505	510	
Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	515	520	525	
Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	530	535	540	
Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	545	550	555	560
Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	565	570	575	
Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	580	585	590	
Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	595	600	605	
Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	610	615	620	

Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	
625							630			635					640	
Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	
				645					650						655	
Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	
			660					665							670	
Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	
			675					680							685	
Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	
			690					695							700	
Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	
			705				710				715				720	
Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	
				725					730						735	
Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys	Phe	Gln	Gln	
			740					745							750	
Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln	Lys	Gln	Lys	
			755					760							765	
Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys				
			770					775							780	

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCGTC	ATG	CCG	CCC	AAA	ACC	CCC	CGA	AAA	ACG	GCC	GCC	ACC	GCC	GCC		48
	Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala		
	1				5					10						
GCT	GCC	GCC	GCG	GAA	CCC	CCG	GCA	CCG	CCG	CCG	CCC	CCT	CCT	GAG		96
Ala	Ala	Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Glu		
	15				20					25				30		

GTC GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	144
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
35 40 45	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	192
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
50 55 60	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	240
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
65 70 75	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	288
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
80 85 90	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	336
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
95 100 105 110	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	384
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
115 120 125	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	432
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
130 135 140	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	480
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
145 150 155	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	528
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
160 165 170	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	576
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
175 180 185 190	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	624
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
195 200 205	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	672
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
210 215 220	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	720
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
225 230 235	

AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu 240 245 250	768
GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser 255 260 265 270	816
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp 275 280 285	864
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met 290 295 300	912
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln 305 310 315	960
CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro 320 325 330	1008
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys 335 340 345 350	1056
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser 355 360 365	1104
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser 370 375 380	1152
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys 385 390 395	1200
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu 400 405 410	1248
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp 415 420 425 430	1296
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu 435 440 445	1344

AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu 450 455 460	1392
GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His 465 470 475	1440
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp 480 485 490	1488
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu 495 500 505 510	1536
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala 515 520 525	1584
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr 530 535 540	1632
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala 545 550 555	1680
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr 560 565 570	1728
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu 575 580 585 590	1776
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu 595 600 605	1824
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His 610 615 620	1872
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys 625 630 635	1920
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu 640 645 650	1968

CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu 655 660 665 670	2016
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg 675 680 685	2064
CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu 690 695 700	2112
TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser 705 710 715	2160
CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser 720 725 730	2208
CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro 735 740 745 750	2256
AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu 755 760 765	2304
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu 770 775 780	2352
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu 785 790 795	2400
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu 800 805 810	2448
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr 815 820 825 830	2496
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser 835 840 845	2544
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT Asn Lys Glu Glu Lys 850	2599
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC	2659

ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA	2719
TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGGTGA	2779
AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG	2839
CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC	2899
TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT	2959
GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAAATG TGTCTATCT ATCTTCCAAA	3019
TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT	3079
ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG	3139
AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA	3199
AGCAAAGTAT AACCATATGA TACTATCATA CTA CTGAAAC AGATTTTATA CCTCAGAATG	3259
TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA	3319
TAGT	3323

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala	
1 5 10 15	
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Val Asp	
20 25 30	
Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu	
35 40 45	
Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser	
50 55 60	
Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val	
65 70 75 80	
Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr	
85 90 95	

Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	100	105	110
Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	115	120	125
Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	130	135	140
Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	145	150	155
Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	165	170	175
Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	180	185	190
Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	195	200	205
Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	210	215	220
Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	225	230	235
Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	245	250	255
Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	260	265	270
Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	275	280	285
Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	290	295	300
Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	305	310	315
Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	325	330	335
Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	340	345	350
Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	355	360	365
Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	370	375	380

Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	385	390	395	400
Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	405	410	415	
Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	420	425	430	
Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	435	440	445	
Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	450	455	460	
Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	465	470	475	480
Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	485	490	495	
Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	500	505	510	
Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	515	520	525	
Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	530	535	540	
Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	545	550	555	560
Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	565	570	575	
Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	580	585	590	
Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	595	600	605	
His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	610	615	620	
Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	625	630	635	640
Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	645	650	655	
Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	660	665	670	

Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys
 675 680 685
 Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro
 690 695 700
 Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu
 705 710 715 720
 Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr
 725 730 735
 Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser
 740 745 750
 Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe
 755 760 765
 Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg
 770 775 780
 Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe
 785 790 795 800
 Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly
 805 810 815
 Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr
 820 825 830
 Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys
 835 840 845
 Glu Glu Lys
 850

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC
 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala
 1 5 10

GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTG GTC GAC	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Val Asp	
65 70 75	
CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA	288
Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu	
80 85 90	
ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT	336
Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser	
95 100 105 110	
ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA	384
Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val	
115 120 125	
TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT	432
Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr	
130 135 140	
TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG	480
Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu	
145 150 155	
GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA	528
Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val	
160 165 170	
TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT	576
Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys	
175 180 185 190	
GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA	624
Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu	
195 200 205	
CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC	672
Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro	
210 215 220	

AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT	720
Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn	
225 230 235	
GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA	768
Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile	
240 245 250	
GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT	816
Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn	
255 260 265 270	
TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT	864
Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu	
275 280 285	
TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA	912
Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala	
290 295 300	
AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC	960
Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp	
305 310 315	
AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG	1008
Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu	
320 325 330	
GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT	1056
Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr	
335 340 345 350	
ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA	1104
Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser	
355 360 365	
GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA	1152
Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu	
370 375 380	
AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA	1200
Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys	
385 390 395	
TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA	1248
Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg	
400 405 410	
TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT	1296
Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu	
415 420 425 430	

AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG	1344
Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu	
435 440 445	
AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT	1392
Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val	
450 455 460	
GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA	1440
Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly	
465 470 475	
ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC	1488
Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala	
480 485 490	
TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC	1536
Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn	
495 500 505 510	
TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC	1584
Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile	
515 520 525	
ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT	1632
Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile	
530 535 540	
AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT	1680
Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala	
545 550 555	
TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG	1728
Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met	
560 565 570	
TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT	1776
Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg	
575 580 585 590	
GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG	1824
Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln	
595 600 605	
ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA	1872
Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys	
610 615 620	
GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT	1920
Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu	
625 630 635	

CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln 640 645 650	1968
CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp 655 660 665 670	2016
CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile 675 680 685	2064
GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His 690 695 700	2112
GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr 705 710 715	2160
GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys 720 725 730	2208
ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro 735 740 745 750	2256
ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu 755 760 765	2304
CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr 770 775 780	2352
AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser 785 790 795	2400
AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe 800 805 810	2448
CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg 815 820 825 830	2496
AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe 835 840 845	2544

GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly 850 855 860	2592
GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr 865 870 875	2640
CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys 880 885 890	2688
GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT Glu Glu Lys 895	2737
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC	2797
ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAAATGTGC AGATGCAATT GTTTGGGTGA	2857
TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA	2917
AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG	2977
CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC	3037
TACTTTGCCT TCTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT	3097
GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGCCTATCT ATCTTCCAAA	3157
TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT	3217
ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG	3277
AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA	3337
AGCAAAGTAT AACCATATGA TACTATCATA CTAAGTAAAC AGATTTTATA CCTCAGAATG	3397
TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA	3457
TAGT	3461

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	
1				5					10					15		
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	
			20					25					30			
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	
		35					40					45				
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	
	50					55					60					
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Val	Asp	Leu	Asp	
65					70				75					80		
Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	
				85					90					95		
Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	
			100					105					110			
Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	
		115					120					125				
Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	
	130					135					140					
Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	
145					150					155				160		
Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	
				165					170					175		
Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	
			180					185					190			
Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	
		195					200					205				
Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	
	210					215					220					
Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	
225					230					235				240		
Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	
				245					250					255		
Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	
			260					265						270		

Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys
275 280 285

Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu
290 295 300

Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe
305 310 315 320

Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn
325 330 335

Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln
340 345 350

Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn
355 360 365

Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile
370 375 380

Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala
385 390 395 400

Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys
405 410 415

Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser
420 425 430

Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp
435 440 445

Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met
450 455 460

Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp
465 470 475 480

Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp
485 490 495

Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr
500 505 510

Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu
515 520 525

Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln
530 535 540

Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro
545 550 555 560

Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	565	570	575
Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	580	585	590
Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	595	600	605
Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	610	615	620
Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	625	630	635
Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	645	650	655
Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	660	665	670
Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	675	680	685
Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	690	695	700
Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	705	710	715
Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	725	730	735
Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	740	745	750
His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	755	760	765
Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	770	775	780
Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	785	790	795
Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	805	810	815
Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	820	825	830
Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	835	840	845

Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser
 850 855 860

Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met
 865 870 875 880

Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu
 885 890 895

Lys

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	

AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GTC GAA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT TCT TGG	384
Val Glu Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val Ser Trp	
115 120 125	
ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA GAT GAT	432
Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu Asp Asp	
130 135 140	
CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT TTT ATT	480
Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr Phe Ile	
145 150 155	
AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA GCT GTT	528
Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr Ala Val	
160 165 170	
ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG	576
Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg	
175 180 185 190	
AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA	624
Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu	
195 200 205	
GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT	672
Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val	
210 215 220	
TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA	720
Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr	
225 230 235	
TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA	768
Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu	
240 245 250	
ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT	816
Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His	
255 260 265 270	
GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA	864
Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg	
275 280 285	
ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA	912
Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro	
290 295 300	

CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	AAC	ACT	ATC	CAA	CAA	TTA	ATG	ATG	960
His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	
		305					310					315				
ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	CCT	TCA	GAA	AAT	CTG	ATT	TCC	TAT	1008
Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	
		320					325					330				
TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	AAA	GAA	AGT	ATA	CTG	AAA	AGA	GTG	1056
Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	
		335					340					345			350	
AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	GAG	AAA	TTT	GCT	AAA	GCT	GTG	GGA	1104
Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	
				355						360					365	
CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	CAG	CGA	TAC	AAA	CTT	GGA	GTT	CGC	1152
Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	
			370						375					380		
TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	ATG	CTT	AAA	TCA	GAA	GAA	GAA	CGA	1200
Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	
			385					390					395			
TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA	CTT	CTG	AAT	GAC	AAC	ATT	TTT	CAT	1248
Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	
		400					405					410				
ATG	TCT	TTA	TTG	GCG	TGC	GCT	CTT	GAG	GTT	GTA	ATG	GCC	ACA	TAT	AGC	1296
Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	
					420					425					430	
AGA	AGT	ACA	TCT	CAG	AAT	CTT	GAT	TCT	GGA	ACA	GAT	TTG	TCT	TTC	CCA	1344
Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	
				435						440					445	
TGG	ATT	CTG	AAT	GTG	CTT	AAT	TTA	AAA	GCC	TTT	GAT	TTT	TAC	AAA	GTG	1392
Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	
			450						455					460		
ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	GGC	AAC	TTG	ACA	AGA	GAA	ATG	ATA	1440
Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	
			465					470					475			
AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	CGA	ATC	ATG	GAA	TCC	CTT	GCA	TGG	1488
Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	
			480					485					490			
CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	CTT	ATT	AAA	CAA	TCA	AAG	GAC	CGA	1536
Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	
					500					505					510	

GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT	1584
Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro	
515 520 525	
CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA	1632
Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg	
530 535 540	
TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT	1680
Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn	
545 550 555	
GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA	1728
Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys	
560 565 570	
TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT	1776
Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr	
575 580 585 590	
CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA	1824
Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu	
595 600 605	
TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG	1872
Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu	
610 615 620	
TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC	1920
Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser	
625 630 635	
ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC	1968
Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile	
640 645 650	
ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC	2016
Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe	
655 660 665 670	
AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC	2064
Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe	
675 680 685	
TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT	2112
Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr	
690 695 700	
GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA	2160
Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg	
705 710 715	

AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC	2208
Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn	
720 725 730	
ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG	2256
Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu	
735 740 745 750	
CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT	2304
Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile	
755 760 765	
GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG	2352
Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met	
770 775 780	
GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC	2400
Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn	
785 790 795	
CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT	2448
Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp	
800 805 810	
GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG	2496
Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln	
815 820 825 830	
AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA	2544
Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys	
835 840 845	
ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC	2593
Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
850 855	
AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT	2653
ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA	2713
TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG	2773
TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT TGTAGCAGAT	2833
TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT	2893
GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG	2953
ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC	3013
TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC ATTCACCAAA	3073
ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT	3133

TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTTATAA 3193
 AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA 3253
 CTACTGAAAC AGATTTTCATA CCTCAGAAATG TAAAAGAACT TACTGATTAT TTTCTTCATC 3313
 CAACTTATGT TTTTAAATGA GGATTATTGA TAGT 3347

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	1	5	10	15
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	20	25	30	
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	35	40	45	
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	50	55	60	
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	65	70	75	80
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	85	90	95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Val	Glu	100	105	110	
Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	115	120	125	
Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	130	135	140	
Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	145	150	155	160
Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	165	170	175	

Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala
180 185 190

Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu Val Leu
195 200 205

Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val Tyr Phe
210 215 220

Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser Asn
225 230 235 240

Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr
245 250 255

Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp Lys
260 265 270

Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro
275 280 285

Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr
290 295 300

Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu
305 310 315 320

Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn
325 330 335

Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp
340 345 350

Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly
355 360 365

Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr
370 375 380

Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser
385 390 395 400

Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser
405 410 415

Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser
420 425 430

Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile
435 440 445

Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu
450 455 460

Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	465	470	475	480
Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	485	490	495	
Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	500	505	510	
Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	515	520	525	
Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	530	535	540	
Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	545	550	555	560
Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	565	570	575	
Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	580	585	590	
Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	595	600	605	
His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	610	615	620	
Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	625	630	635	640
Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	645	650	655	
Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	660	665	670	
Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	675	680	685	
Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	690	695	700	
Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	705	710	715	720
Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	725	730	735	
Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	740	745	750	

Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu
 755 760 765
 Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys
 770 775 780
 Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro
 785 790 795 800
 Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala
 805 810 815
 Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu
 820 825 830
 Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn
 835 840 845
 Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
 850 855

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	

AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG	384
Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln	
115 120 125	
AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT	432
Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile	
130 135 140	
ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA	480
Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys	
145 150 155	
AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT	528
Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu	
160 165 170	
GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC	576
Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr	
175 180 185 190	
GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG	624
Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu	
195 200 205	
GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA	672
Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr	
210 215 220	
CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT	720
Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile	
225 230 235	
CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA	768
Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu	
240 245 250	
ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT	816
Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile	
255 260 265 270	

TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA	864
Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys	
275 280 285	
AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT	912
Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala	
290 295 300	
GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA	960
Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly	
305 310 315	
GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA	1008
Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu	
320 325 330	
GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT	1056
Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile	
335 340 345 350	
TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA	1104
Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr	
355 360 365	
TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT	1152
Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser	
370 375 380	
TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC	1200
Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr	
385 390 395	
AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA	1248
Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu	
400 405 410	
ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT	1296
Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu	
415 420 425 430	
GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG	1344
Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys	
435 440 445	
GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT	1392
Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn	
450 455 460	
CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT	1440
Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro	
465 470 475	

GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT	1488
Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr	
480 485 490	
GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA	1536
Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro	
495 500 505 510	
TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA	1584
Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu	
515 520 525	
GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC	1632
Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His	
530 535 540	
CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG	1680
Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln	
545 550 555	
AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG	1728
Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met	
560 565 570	
TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC	1776
Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe	
575 580 585 590	
AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG	1824
Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu	
595 600 605	
ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA	1872
Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile	
610 615 620	
GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG	1920
Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu	
625 630 635	
CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT	1968
Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile	
640 645 650	
CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA	2016
Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly	
655 660 665 670	
GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA	2064
Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu	
675 680 685	

GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val 690 695 700	2112
TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn 705 710 715	2160
CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly 720 725 730	2208
AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly 735 740 745 750	2256
TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe 755 760 765	2304
CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys 770 775 780	2352
CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys 785 790 795	2397
TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG	2457
ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT	2517
TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG	2577
TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT	2637
TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG	2697
GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG	2757
CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC	2817
ATGAACACCC TTAGAAAATG TGCCTATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC	2877
ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA	2937
AATTACTAAT TTTACACATT AGATTTTATT TTAATTATTGG AATCTGATAT ACTGTGTGCT	2997
TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA	3057
TACTATCATA CTAAGTAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT TACTGATTAT	3117
TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3161

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
1 5 10 15

Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
20 25 30

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
35 40 45

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
50 55 60

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65 70 75 80

Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
85 90 95

Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Ala Val
100 105 110

Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg
115 120 125

Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu
130 135 140

Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val
145 150 155 160

Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr
165 170 175

Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu
180 185 190

Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His
195 200 205

Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg
210 215 220

Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	225	230	235	240
His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	245	250	255	
Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	260	265	270	
Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	275	280	285	
Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	290	295	300	
Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	305	310	315	320
Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	325	330	335	
Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	340	345	350	
Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	355	360	365	
Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	370	375	380	
Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	385	390	395	400
Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	405	410	415	
Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	420	425	430	
Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	435	440	445	
Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	450	455	460	
Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	465	470	475	480
Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	485	490	495	
Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	500	505	510	

Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr
 515 520 525

Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu
 530 535 540

Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu
 545 550 555 560

Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser
 565 570 575

Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile
 580 585 590

Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe
 595 600 605

Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe
 610 615 620

Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr
 625 630 635 640

Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg
 645 650 655

Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn
 660 665 670

Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu
 675 680 685

Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile
 690 695 700

Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met
 705 710 715 720

Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn
 725 730 735

Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp
 740 745 750

Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln
 755 760 765

Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys
 770 775 780

Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
 785 790 795

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	

TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu 160 165 170	528
ACA CAA CCC AGC AGT TCG ATG GTC GCT GTT ATA CCC ATT AAT GGT TCA Thr Gln Pro Ser Ser Ser Met Val Ala Val Ile Pro Ile Asn Gly Ser 175 180 185 190	576
CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys 195 200 205	624
CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His 210 215 220	672
GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA Glu Cys Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile 225 230 235	720
CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu 240 245 250	768
GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys 255 260 265 270	816
GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr 275 280 285	864
GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn 290 295 300	912
CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr 305 310 315	960
GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser 320 325 330	1008
GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val 335 340 345 350	1056
AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile 355 360 365	1104

TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT	1152
Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile	
370 375 380	
GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG	1200
Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met	
385 390 395	
GAA TCC ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT	1248
Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe	
400 405 410	
AGC AAA CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC	1296
Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys	
415 420 425 430	
GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT	1344
Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn	
435 440 445	
CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT	1392
Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu	
450 455 460	
AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA	1440
Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys	
465 470 475	
GCA GAA GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT	1488
Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys	
480 485 490	
GAA CAT CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA	1536
Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu	
495 500 505 510	
TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC	1584
Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His	
515 520 525	
CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT	1632
Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr	
530 535 540	
GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT	1680
Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly	
545 550 555	
TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC	1728
Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr	
560 565 570	

TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG	1776
Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu	
575 580 585 590	
TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT	1824
Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu	
595 600 605	
TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG	1872
Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp	
610 615 620	
ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC	1920
Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp	
625 630 635	
AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA	1968
Arg His Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys	
640 645 650	
GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG	2016
Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys	
655 660 665 670	
GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA	2064
Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys	
675 680 685	
GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG	2112
Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met	
690 695 700	
CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT	2160
Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro	
705 710 715	
ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT	2208
Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro	
720 725 730	
AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG	2256
Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu	
735 740 745 750	
AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG	2304
Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met	
755 760 765	
ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT	2352
Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr	
770 775 780	

TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT	2400
Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg	
785 790 795	
GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA	2448
Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys	
800 805 810	
AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA	2496
Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys	
815 820 825 830	
CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT	2544
His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr	
835 840 845	
TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT	2592
Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp	
850 855 860	
ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT	2643
Thr Ser Asn Lys Glu Glu Lys	
865	
GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT	2703
TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT	2763
GTTTGGGTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA	2823
ATCTTG TGTA AATCCTGCCA TTAAAAAGT TG TAGCAGAT TGTTTCCTCT TCCAAAGTAA	2883
AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG	2943
CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT	3003
TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT	3063
ATCTTCCAAA TGCAATTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC	3123
AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT	3183
TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTATAA AATTTTGCTT TTAATTAAAT	3243
AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA	3303
CCTCAGAATG TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA	3363
GGATTATTGA TAGT	3377

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	
1				5					10					15		
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	
			20					25					30			
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	
		35					40					45				
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	
	50					55					60					
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	
65					70				75					80		
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	
			85						90					95		
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	
		100						105					110			
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	
		115					120					125				
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	
	130					135					140					
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	
145					150					155				160		
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	
			165						170					175		
Pro	Ser	Ser	Ser	Met	Val	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	
			180					185					190			
Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	
		195				200						205				
Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	
	210					215					220					

Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	
225					230					235					240	
Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	
			245						250					255		
Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	
			260					265						270		
Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	
		275					280							285		
Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	
	290					295					300					
Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	
305					310					315					320	
Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	
			325						330						335	
Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	
			340					345						350		
Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	
	355						360					365				
Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	
	370					375				380						
Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	
385				390						395					400	
Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	
			405						410						415	
Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	
		420						425						430		
Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	
	435						440							445		
Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	
	450					455					460					
Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	
465					470					475					480	
Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	
			485						490					495		
Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	
		500						505						510		

Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	515	520	525	
Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	530	535	540	
Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	545	550	555	560
Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	565	570	575	
Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	580	585	590	
Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	595	600	605	
Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	610	615	620	
Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	625	630	635	640
Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	645	650	655	
Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	660	665	670	
Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	675	680	685	
Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	690	695	700	
Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	705	710	715	720
Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	725	730	735	
Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	740	745	750	
Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	755	760	765	
Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	770	775	780	
Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	785	790	795	800

AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	576
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
175 180 185 190	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	624
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
195 200 205	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	672
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
210 215 220	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	720
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
225 230 235	
TAT AAA ACA GGG TCG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT	768
Tyr Lys Thr Gly Ser Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu	
240 245 250	
CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA	816
Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys	
255 260 265 270	
AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT	864
Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu	
275 280 285	
CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA	912
Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys	
290 295 300	

AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT	960
Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val	
305 310 315	
AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA	1008
Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser	
320 325 330	
GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC	1056
Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys	
335 340 345 350	
ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA	1104
Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly	
355 360 365	
TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC	1152
Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val	
370 375 380	
GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA	1200
Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg	
385 390 395	
GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA	1248
Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln	
400 405 410	
AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG	1296
Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu	
415 420 425 430	
GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT	1344
Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser	
435 440 445	
CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT	1392
Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn	
450 455 460	
GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT	1440
Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe	
465 470 475	
ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA	1488
Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu	
480 485 490	
CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA	1536
Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser	
495 500 505 510	

CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT	1584
Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr	
515 520 525	
GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT	1632
Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn	
530 535 540	
CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA	1680
His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys	
545 550 555	
AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA	1728
Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln	
560 565 570	
GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT	1776
Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu	
575 580 585 590	
TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT	1824
Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn	
595 600 605	
ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC	1872
Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile	
610 615 620	
ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG	1920
Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met	
625 630 635	
AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA	1968
Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile	
640 645 650	
TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA	2016
Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala	
655 660 665 670	
TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG	2064
Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu	
675 680 685	
ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC	2112
Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val	
690 695 700	
TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG	2160
Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg	
705 710 715	

CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys 720 725 730	2208
TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser 735 740 745 750	2256
CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr 755 760 765	2304
AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe 770 775 780	2352
GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser 785 790 795	2400
GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro 800 805 810	2448
CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly 815 820 825 830	2496
AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu 835 840 845	2544
ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser 850 855 860	2592
ATG GAT ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG Met Asp Thr Ser Asn Lys Glu Glu Lys 865 870	2639
TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACCTTCC	2699
CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAATGTGC	2759
AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC	2819
AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT	2879
TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG	2939
ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC	2999
TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG	3059

TGTCCTATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA	3119
ACTCTTCTGC AAAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT	3179
AGATTTTATT TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT	3239
TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA CTA CTGAAAC	3299
AGATTTTCATA CCTCAGAATG TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT	3359
TTTTAAATGA GGATTATTGA TAGT	3383

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	1	5	10	15
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	20	25	30	
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	35	40	45	
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	50	55	60	
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	65	70	75	80
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	85	90	95	
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	100	105	110	
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	115	120	125	
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	130	135	140	
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	145	150	155	160

Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	165	170	175	
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	180	185	190	
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	195	200	205	
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	210	215	220	
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	225	230	235	240
Thr	Gly	Ser	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	245	250	255	
Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	260	265	270	
Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	275	280	285	
Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	290	295	300	
Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	305	310	315	320
Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	325	330	335	
Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	340	345	350	
Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	355	360	365	
Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	370	375	380	
Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	385	390	395	400
Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	405	410	415	
Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	420	425	430	
Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	435	440	445	

Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu		
450						455					460						
Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys		
465					470					475					480		
Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys		
			485						490					495			
Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu		
			500					505					510				
Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His		
		515					520					525					
Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr		
	530					535					540						
Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly		
545					550					555					560		
Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr		
			565					570						575			
Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu		
			580					585					590				
Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu		
		595					600					605					
Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp		
	610					615					620						
Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp		
625					630					635					640		
Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys		
			645					650						655			
Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys		
		660						665					670				
Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys		
		675					680					685					
Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met		
	690					695					700						
Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro		
705					710					715					720		
Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro		
			725					730						735			

Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu
 740 745 750
 Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met
 755 760 765
 Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr
 770 775 780
 Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg
 785 790 795 800
 Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys
 805 810 815
 Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys
 820 825 830
 His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr
 835 840 845
 Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp
 850 855 860
 Thr Ser Asn Lys Glu Glu Lys
 865 870

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	

CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GGT GAT ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Gly Asp Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	576
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
175 180 185 190	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	624
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
195 200 205	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	672
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
210 215 220	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	720
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
225 230 235	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	768
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
240 245 250	

CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	816
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
255 260 265 270	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	864
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
275 280 285	
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT	912
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser	
290 295 300	
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT	960
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser	
305 310 315	
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA	1008
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg	
320 325 330	
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT	1056
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser	
335 340 345 350	
TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG	1104
Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val	
355 360 365	
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC	1152
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile	
370 375 380	
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA	1200
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu	
385 390 395	
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT	1248
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser	
400 405 410	
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT	1296
Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe	
415 420 425 430	
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC	1344
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr	
435 440 445	
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA	1392
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys	
450 455 460	

TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT	1440
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn	
465 470 475	
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA	1488
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val	
480 485 490	
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA	1536
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr	
495 500 505 510	
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT	1584
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe	
515 520 525	
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1632
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
530 535 540	
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1680
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
545 550 555	
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1728
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
560 565 570	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1776
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
575 580 585 590	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1824
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
595 600 605	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1872
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
610 615 620	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1920
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
625 630 635	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1968
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
640 645 650	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	2016
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
655 660 665 670	

TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	2064
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
675 680 685	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	2112
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
690 695 700	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	2160
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
705 710 715	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	2208
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
720 725 730	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	2256
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
735 740 745 750	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	2304
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
755 760 765	
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA	2352
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile	
770 775 780	
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2400
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg	
785 790 795	
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA	2448
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys	
800 805 810	
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA	2496
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg	
815 820 825 830	
ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG	2544
Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln	
835 840 845	
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT	2592
Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser	
850 855 860	
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT	2640
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp	
865 870 875	

ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu 880 885 890	2688
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg 895 900 905 910	2736
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu 915 920 925	2784
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG Glu Lys	2840
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2900
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2960
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	3020
TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	3080
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3140
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	3200
TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCCTATCT ATCTTCCAAA TGCAATTGTA	3260
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	3320
ATTAGAAAAA AATTACTAAT TTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3380
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT	3440
AACCATATGA TACTATCATA CTA CTACTGAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT	3500
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3554

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala
1					5				10					15	

Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp
 20 25 30
 Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
 35 40 45
 Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
 50 55 60
 Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
 65 70 75 80
 Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
 85 90 95
 Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Gly Asp
 100 105 110
 Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
 115 120 125
 His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
 130 135 140
 Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
 145 150 155 160
 Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
 165 170 175
 Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
 180 185 190
 Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
 195 200 205
 Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
 210 215 220
 Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
 225 230 235 240
 Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
 245 250 255
 Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
 260 265 270
 Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
 275 280 285
 Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
 290 295 300

Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305 310 315 320

Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
325 330 335

Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
340 345 350

Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
355 360 365

Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
370 375 380

Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385 390 395 400

Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
405 410 415

Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
420 425 430

Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
435 440 445

Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
450 455 460

Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
465 470 475 480

Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
485 490 495

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
500 505 510

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
515 520 525

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
530 535 540

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545 550 555 560

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
565 570 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
580 585 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
595 600 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
610 615 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625 630 635 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
645 650 655

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
660 665 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
675 680 685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
690 695 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705 710 715 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
725 730 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
740 745 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
755 760 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
770 775 780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785 790 795 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
805 810 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
820 825 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
835 840 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
850 855 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865 870 875 880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
885 890 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
900 905 910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
915 920 925